

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 2, 2002, 08:21:53 ; Search time 28.78 Seconds
 (without alignments)
 15.438 Million cell updates/sec

Title: US-09-781-133-1
Perfect score: 20
Sequence: 1 LVFF 4

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 135323

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

Database : A_Geneseq_032802:*

- 1: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
- 2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
- 3: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
- 4: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
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- 13: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*
- 14: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
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 21: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2000.DAT:*
 22: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match	Length	DB	ID	Description
	Score						
1	20	100.0	4	17	AAW02317	Beta-amyloid modul	
2	20	100.0	4	18	AAW45955	Amyloid beta pepti	
3	20	100.0	4	19	AAW51318	Peptide #1 useful	
4	20	100.0	4	19	AAW47234	Beta-amyloid pepti	
5	20	100.0	4	20	AAW89364	Beta-amyloid pepti	
6	20	100.0	4	21	AAB27021	Beta-amyloid pepti	
7	20	100.0	4	21	AAY49973	Natural beta amylo	
8	20	100.0	4	22	AAE12515	Beta-amyloid precu	
9	20	100.0	4	22	AAE12517	APP 770 Abeta pept	
10	20	100.0	4	22	AAE09985	Beta-amyloid pepti	
11	20	100.0	5	16	AAR87922	Test peptide used	
12	20	100.0	5	17	AAW02322	Beta-amyloid modul	
13	20	100.0	5	17	AAW02332	Beta-amyloid modul	
14	20	100.0	5	17	AAW02315	Beta-amyloid modul	
15	20	100.0	5	17	AAW02316	Beta-amyloid modul	
16	20	100.0	5	18	AAW45933	Partial sequence o	
17	20	100.0	5	18	AAW45962	Peptide derived fr	
18	20	100.0	5	19	AAW51340	Peptide #23 useful	
19	20	100.0	5	19	AAW51322	Peptide #5 useful	
20	20	100.0	5	19	AAW51335	Peptide #18 useful	
21	20	100.0	5	19	AAW51339	Peptide #22 useful	
22	20	100.0	5	19	AAW51341	Peptide #24 useful	
23	20	100.0	5	19	AAW51342	Peptide #25 useful	
24	20	100.0	5	20	AAW29089	A-beta-binding pep	
25	20	100.0	5	20	AAW89389	Beta-amyloid pepti	
26	20	100.0	5	20	AAW89367	Beta-amyloid pepti	
27	20	100.0	5	20	AAW89381	Beta-amyloid pepti	
28	20	100.0	5	20	AAW89365	Beta-amyloid pepti	

29	20	100.0	5	21	AAB27022	Beta-amyloid pepti
30	20	100.0	5	21	AAB27025	Beta-amyloid pepti
31	20	100.0	5	21	AAB27035	Beta-amyloid pepti
32	20	100.0	5	21	AAAY79937	Beta-amyloid recog
33	20	100.0	5	21	AAAY49979	Natural beta amylo
34	20	100.0	5	21	AAAY49994	Natural beta amylo
35	20	100.0	5	21	AAAY49997	Natural beta amylo
36	20	100.0	5	21	AAAY50000	Natural beta amylo
37	20	100.0	5	21	AAAY56101	Natural beta amylo
38	20	100.0	5	22	AAE12510	Beta-amyloid precu
39	20	100.0	5	22	AAE12522	APP 770 Abeta pept
40	20	100.0	5	22	AAE12533	APP70 abeta peptid
41	20	100.0	5	22	AAE12534	APP70 abeta peptid
42	20	100.0	5	22	AAE12549	Peptide #3 for ana
43	20	100.0	5	22	AAB82629	All-D peptide used
44	20	100.0	5	22	AAB82637	All-D peptide used
45	20	100.0	5	22	AAB82644	All-D peptide used
46	20	100.0	5	22	AAB82645	All-D peptide used
47	20	100.0	5	22	AAB82646	All-D peptide used
48	20	100.0	5	22	AAB82647	All-D peptide used
49	20	100.0	5	22	AAB82648	All-D peptide used
50	20	100.0	5	22	AAB82649	All-D peptide used
51	20	100.0	5	22	AAB62803	Residues 16-20 of
52	20	100.0	5	22	AAB67279	Residues 16-20 of
53	20	100.0	5	22	AAB48481	Antifibrillogenic
54	20	100.0	5	22	AAB48489	Antifibrillogenic
55	20	100.0	5	22	AAE09986	Beta-amyloid pepti
56	20	100.0	5	22	AAE10008	Beta-amyloid pepti
57	20	100.0	5	22	AAE10009	Beta-amyloid pepti
58	20	100.0	5	22	AAE10010	Beta-amyloid pepti
59	20	100.0	5	22	AAE10011	Beta-amyloid pepti
60	20	100.0	5	22	AAE10176	Beta-amyloid pepti
61	20	100.0	5	22	AAE10177	Beta-amyloid pepti
62	20	100.0	6	17	AAW02327	Beta-amyloid modul
63	20	100.0	6	17	AAW02331	Beta-amyloid modul
64	20	100.0	6	17	AAW02313	Beta-amyloid modul
65	20	100.0	6	17	AAW02314	Beta-amyloid modul
66	20	100.0	6	18	AAW45944	Amyloid beta pepti
67	20	100.0	6	20	AAW29090	A-beta-binding pep
68	20	100.0	6	20	AAW29091	A-beta-binding pep
69	20	100.0	6	20	AAW29092	A-beta-binding pep
70	20	100.0	6	20	AAW89385	Beta-amyloid pepti
71	20	100.0	6	20	AAW89388	Beta-amyloid pepti
72	20	100.0	6	20	AAW89377	Beta-amyloid pepti
73	20	100.0	6	20	AAW89378	Beta-amyloid pepti

74	20	100.0	6	21	AAB27036	Beta-amyloid pepti
75	20	100.0	6	21	AAB27045	Beta-amyloid pepti
76	20	100.0	6	22	AAB82632	All-D peptide used
77	20	100.0	6	22	AAB48476	Antifibrillogenic
78	20	100.0	6	22	AAB48484	Antifibrillogenic
79	20	100.0	6	22	AAB48496	Antifibrillogenic
80	20	100.0	7	14	AAR45231	Beta amyloid prote
81	20	100.0	7	14	AAR45232	Beta amyloid prote
82	20	100.0	7	14	AAR45233	Beta amyloid prote
83	20	100.0	7	16	AAR87921	Test peptide used
84	20	100.0	7	16	AAR88300	Non-amnestic pepti
85	20	100.0	7	17	AAW02311	Beta-amyloid modul
86	20	100.0	7	17	AAW02312	Beta-amyloid modul
87	20	100.0	7	18	AAW45940	Amyloid beta pepti
88	20	100.0	7	20	AAW89375	Beta-amyloid pepti
89	20	100.0	7	20	AAW89376	Beta-amyloid pepti
90	20	100.0	7	22	AAB82624	All-D peptide used
91	20	100.0	7	22	AAB82639	All-D peptide used
92	20	100.0	7	22	AAB82640	All-D peptide used
93	20	100.0	7	22	AAB67281	Residues 16-22 of
94	20	100.0	7	22	AAB48475	Antifibrillogenic
95	20	100.0	7	22	AAB48491	Antifibrillogenic
96	20	100.0	7	22	AAB48492	Antifibrillogenic
97	20	100.0	8	11	AAR08190	Cerebrovascular am
98	20	100.0	8	17	AAW02310	Beta-amyloid modul
99	20	100.0	8	18	AAW45937	Amyloid beta pepti
100	20	100.0	8	18	AAW45967	Peptide derived fr

ALIGNMENTS

RESULT 1

AAW02317

ID AAW02317 standard; peptide; 4 AA.

XX

AC AAW02317;

XX

DT 02-MAY-1997 (first entry)

XX

DE Beta-amyloid modulator peptide #8.

XX

KW Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;

KW cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;

KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;

KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;
KW bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;
KW adult-onset diabetes; familial Mediterranean fever; therapy; deafness;
KW scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
PN WO9628471-A1.
XX
PD 19-SEP-1996.
XX
PF 14-MAR-1996; 96WO-US03492.
XX
PR 27-OCT-1995; 95US-0548998.
PR 14-MAR-1995; 95US-0404831.
PR 07-JUN-1995; 95US-0475579.
XX
PA (PHAR-) PHARM PEPTIDES INC.
XX
PI Benjamin H, Chin J, Findeis MA, Garnick MB, Geftter ML;
PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;
PI Molineaux S, Musso G, Reed MJ, Signer ER, Wakefield J;
XX
DR WPI; 1996-433762/43.
XX
PT Modulators of amyloid aggregation - comprising, e.g. amyloidogenic
PT protein coupled (in)directly to at least 1 modifying gp., useful in
PT treatment of Alzheimer's disease
XX
PS Claim 16; Page 91; 106pp; English.
XX
CC AAW02310-W02332 represent the peptide portions of the beta-amyloid
CC modulator compounds of the invention. Beta-amyloid peptide is a 4
CC kilodalton peptide that is the major protein component of amyloid
CC plaques. Amyloid plaques are present both in the brain lesions, and in
CC the walls of cerebral blood vessels in Alzheimer's disease patients.
CC The amyloid modulators of the invention comprise an amyloidogenic protein
CC or peptide (such as this sequence) coupled directly or indirectly to at
CC least one modifying group. The modifying group is preferably a cyclic,
CC heterocyclic, or polycyclic group, such as declain, a cholanyl group, a
CC biotin containing group, or a fluorescein containing group. These
CC compounds then modulate the aggregation of these sequences to natural
CC amyloid proteins or peptides when contacted with the natural
CC amyloidogenic proteins or peptides. The modulator compounds can be used
CC in the treatment of disorders associated with amyloidosis, such as

CC familial amyloid polyneuropathy, familial amyloid cardiomyopathy,
CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,
CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset
CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid
CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage
CC and other types of amyloidosis. The modulators are also useful for the
CC treatment of disorders associated with beta-amyloidosis, especially
CC Alzheimer's disease.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 17; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFF 4
|||
Db 1 lvff 4

RESULT 2

AAW45955

ID AAW45955 standard; peptide; 4 AA.

XX

AC AAW45955;

XX

DT 30-JUN-1998 (first entry)

XX

DE Amyloid beta peptide fragment.

XX

KW Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;

KW positron emission tomography; PET; Down's syndrome; amyloidosis.

XX

OS Homo sapiens.

XX

PN WO9721728-A1.

XX

PD 19-JUN-1997.

XX

PF 09-DEC-1996; 96WO-SE01621.

XX

PR 29-DEC-1995; 95US-0009386.

PR 12-DEC-1995; 95SE-0004467.

XX

PA (KARO-) KAROLINSKA INNOVATIONS AB.

XX

PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;

XX

DR WPI; 1997-332723/30.

XX

PT Use of new and known peptide(s) for inhibition of polymerisation of

PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or

PT Down's syndrome associated with amyloidosis.

XX

PS Example 1; Figure 2B; 31pp; English.

XX

CC This sequence represents a fragment of the amyloid beta peptide. The
CC invention relates to the use of peptide compounds for inhibition of
CC polymerisation of amyloid beta peptide (ABP), as model substances for
CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
CC tool for the identification of other organic compounds with similar
CC functional properties, or as ligands in positron emission tomography.
CC The peptides may be used in treatment of amyloidosis, especially in
CC treatment of Alzheimer's disease associated with amyloidosis, for
CC treatment or prevention of demens in patients with Down's syndrome, for
CC treatment or prevention of hereditary cerebral haemorrhage with
CC amyloidosis (Dutch type) or for the prevention of fibril formation of
CC human amyloid protein. They can also be used for identifying other
CC molecules with similar properties and/or as ligands for detection of
CC amyloid deposits using e.g. positron emission tomography.

XX

SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 18; Length 4;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFF 4

||||

Db 1 lvff 4

RESULT 7

AAY49973

ID AAY49973 standard; peptide; 4 AA.

XX

AC AAY49973;
XX
DT 04-FEB-2000 (first entry)
XX
DE Natural beta amyloid peptide aggregation modulating peptide #1.
XX
KW Beta amyloid peptide aggregation; modulation; D-amino acid; diagnosis;
KW retro-inverso isomer; amyloidogenic disease; Alzheimer's disease;
KW Down's syndrome; hereditary cerebral haemorrhage; HCHWA-D;
KW amyloidosis-Dutch-type.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..4
FT /note= "D-form residues"
XX
PN US5985242-A.
XX
PD 16-NOV-1999.
XX
PF 27-AUG-1997; 97US-0920162.
XX
PR 27-OCT-1995; 95US-0548998.
PR 14-MAR-1996; 96US-0616081.
PR 27-AUG-1996; 96US-0703675.
PR 21-JUL-1997; 97US-0897342.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PI Wakefield J, Molineaux S, Signer ER, Kelley M, Komar-Panicucci S;
PI Musso G, Phillips K, Hayward NJ, Gefter ML, Findeis MA, Lee J;
PI Arico-Muendel CC, Chin J;
XX
DR WPI; 2000-022266/02.
XX
PT Compound comprising a peptidic structure, an amino-terminal modifying
PT group and a carboxy-terminal modifying group, useful for treating
PT Alzheimer's disease -
XX
PS Claim 1; Column 61; 40pp; English.
XX
CC The present invention describes a compound of formula A-(Xaa)-B,
CC comprising a peptidic structure (Xaa), an amino-terminal modifying

CC group (A), and a carboxy-terminal modifying group (B). AAY49973 to
CC AAY49994 represent specifically claimed examples of (Xaa). Also
CC described is a method for inhibiting aggregation of natural beta-amyloid
CC peptides and treating Alzheimer's disease, comprising contacting the
CC amyloid peptides with A-(Xaa)-B; and a method for detecting the presence
CC of natural beta-amyloid peptides in a biological sample by contacting
CC with A-(Xaa)-B. The compound is useful for treating Alzheimer's disease
CC and for detecting the presence of natural beta-amyloid peptides in a
CC biological sample. The compound can also be used prophylactically or
CC therapeutically to treat other clinical occurrences of beta-amyloid
CC deposition, such as in Down's syndrome individuals and in patients with
CC hereditary cerebral haemorrhage with amyloidosis-Dutch-type (HCHWA-D).
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 21; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFF 4
|||
Db 1 lvff 4

Search completed: October 2, 2002, 08:26:25
Job time: 272 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 2, 2002, 08:24:53 ; Search time 12.86 Seconds
(without alignments)
7.597 Million cell updates/sec

Title: US-09-781-133-1
Perfect score: 20
Sequence: 1 LVFF 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 70601

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued_Patents_AA:*
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID		Description

1	20	100.0	4	1	US-08-304-585-10	Sequence 10, Appl
2	20	100.0	4	2	US-08-612-785B-12	Sequence 12, Appl
3	20	100.0	4	2	US-08-920-162A-8	Sequence 8, Appli
4	20	100.0	4	2	US-08-920-162A-9	Sequence 9, Appli
5	20	100.0	4	4	US-09-356-931-8	Sequence 8, Appli
6	20	100.0	4	4	US-09-356-931-9	Sequence 9, Appli
7	20	100.0	4	4	US-08-703-675C-8	Sequence 8, Appli
8	20	100.0	4	4	US-08-703-675C-9	Sequence 9, Appli
9	20	100.0	4	4	US-09-242-724-29	Sequence 29, Appl
10	20	100.0	4	4	US-08-617-267C-12	Sequence 12, Appl
11	20	100.0	5	1	US-08-127-904-15	Sequence 15, Appl
12	20	100.0	5	2	US-08-612-785B-10	Sequence 10, Appl
13	20	100.0	5	2	US-08-612-785B-11	Sequence 11, Appl
14	20	100.0	5	2	US-08-612-785B-22	Sequence 22, Appl
15	20	100.0	5	2	US-08-612-785B-32	Sequence 32, Appl
16	20	100.0	5	2	US-08-920-162A-3	Sequence 3, Appli
17	20	100.0	5	2	US-08-920-162A-16	Sequence 16, Appl
18	20	100.0	5	2	US-08-920-162A-27	Sequence 27, Appl
19	20	100.0	5	2	US-08-920-162A-28	Sequence 28, Appl
20	20	100.0	5	2	US-08-920-162A-33	Sequence 33, Appl
21	20	100.0	5	2	US-08-920-162A-34	Sequence 34, Appl
22	20	100.0	5	3	US-08-970-833-2	Sequence 2, Appli
23	20	100.0	5	4	US-09-356-931-3	Sequence 3, Appli
24	20	100.0	5	4	US-09-356-931-16	Sequence 16, Appl
25	20	100.0	5	4	US-09-356-931-27	Sequence 27, Appl
26	20	100.0	5	4	US-09-356-931-28	Sequence 28, Appl
27	20	100.0	5	4	US-09-356-931-33	Sequence 33, Appl
28	20	100.0	5	4	US-09-356-931-34	Sequence 34, Appl
29	20	100.0	5	4	US-08-703-675C-3	Sequence 3, Appli
30	20	100.0	5	4	US-08-703-675C-16	Sequence 16, Appl
31	20	100.0	5	4	US-08-703-675C-35	Sequence 35, Appl
32	20	100.0	5	4	US-08-703-675C-45	Sequence 45, Appl
33	20	100.0	5	4	US-08-703-675C-46	Sequence 46, Appl
34	20	100.0	5	4	US-09-242-724-25	Sequence 25, Appl
35	20	100.0	5	4	US-09-242-724-26	Sequence 26, Appl
36	20	100.0	5	4	US-08-617-267C-10	Sequence 10, Appl
37	20	100.0	5	4	US-08-617-267C-11	Sequence 11, Appl
38	20	100.0	5	4	US-08-617-267C-22	Sequence 22, Appl
39	20	100.0	5	4	US-08-617-267C-32	Sequence 32, Appl
40	20	100.0	5	5	PCT-US94-10475-15	Sequence 15, Appl
41	20	100.0	6	2	US-08-612-785B-8	Sequence 8, Appli
42	20	100.0	6	2	US-08-612-785B-9	Sequence 9, Appli
43	20	100.0	6	2	US-08-612-785B-27	Sequence 27, Appl
44	20	100.0	6	2	US-08-612-785B-31	Sequence 31, Appl

45	20	100.0	6 3	US-08-664-379B-19	Sequence 19, Appl
46	20	100.0	6 4	US-08-703-675C-31	Sequence 31, Appl
47	20	100.0	6 4	US-08-703-675C-32	Sequence 32, Appl
48	20	100.0	6 4	US-08-703-675C-40	Sequence 40, Appl
49	20	100.0	6 4	US-08-703-675C-44	Sequence 44, Appl
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52	20	100.0	6 4	US-09-242-724-30	Sequence 30, Appl
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54	20	100.0	6 4	US-09-242-724-33	Sequence 33, Appl
55	20	100.0	6 4	US-08-617-267C-8	Sequence 8, Appli
56	20	100.0	6 4	US-08-617-267C-9	Sequence 9, Appli
57	20	100.0	6 4	US-08-617-267C-27	Sequence 27, Appl
58	20	100.0	6 4	US-08-617-267C-31	Sequence 31, Appl
59	20	100.0	6 4	US-08-617-267C-43	Sequence 43, Appl
60	20	100.0	7 1	US-08-127-904-14	Sequence 14, Appl
61	20	100.0	7 2	US-08-612-785B-6	Sequence 6, Appli
62	20	100.0	7 2	US-08-612-785B-7	Sequence 7, Appli
63	20	100.0	7 4	US-08-703-675C-29	Sequence 29, Appl
64	20	100.0	7 4	US-08-703-675C-30	Sequence 30, Appl
65	20	100.0	7 4	US-08-617-267C-6	Sequence 6, Appli
66	20	100.0	7 4	US-08-617-267C-7	Sequence 7, Appli
67	20	100.0	7 4	US-09-264-709A-13	Sequence 13, Appl
68	20	100.0	7 5	PCT-US94-10475-14	Sequence 14, Appl
69	20	100.0	8 2	US-08-612-785B-5	Sequence 5, Appli
70	20	100.0	8 2	US-08-630-645-1	Sequence 1, Appli
71	20	100.0	8 4	US-08-703-675C-28	Sequence 28, Appl
72	20	100.0	8 4	US-08-617-267C-5	Sequence 5, Appli
73	20	100.0	8 5	PCT-US96-10220-1	Sequence 1, Appli
74	20	100.0	9 4	US-09-264-709A-4	Sequence 4, Appli
75	20	100.0	10 3	US-08-970-833-3	Sequence 3, Appli
76	17	85.0	4 2	US-08-920-162A-11	Sequence 11, Appl
77	17	85.0	4 2	US-08-920-162A-13	Sequence 13, Appl
78	17	85.0	4 4	US-09-356-931-11	Sequence 11, Appl
79	17	85.0	4 4	US-09-356-931-13	Sequence 13, Appl
80	17	85.0	4 4	US-08-703-675C-11	Sequence 11, Appl
81	17	85.0	4 4	US-08-703-675C-13	Sequence 13, Appl
82	17	85.0	5 2	US-08-920-162A-18	Sequence 18, Appl
83	17	85.0	5 2	US-08-920-162A-20	Sequence 20, Appl
84	17	85.0	5 2	US-08-920-162A-32	Sequence 32, Appl
85	17	85.0	5 4	US-09-356-931-18	Sequence 18, Appl
86	17	85.0	5 4	US-09-356-931-20	Sequence 20, Appl
87	17	85.0	5 4	US-09-356-931-32	Sequence 32, Appl
88	17	85.0	5 4	US-08-703-675C-18	Sequence 18, Appl
89	17	85.0	5 4	US-08-703-675C-20	Sequence 20, Appl

90	17	85.0	5	4	US-08-703-675C-27	Sequence 27, Appl
91	17	85.0	9	1	US-07-716-826-4	Sequence 4, Appli
92	17	85.0	9	1	US-08-012-711-4	Sequence 4, Appli
93	16	80.0	3	1	US-08-079-812-139	Sequence 139, App
94	16	80.0	3	2	US-08-612-785B-19	Sequence 19, Appl
95	16	80.0	3	4	US-08-617-267C-19	Sequence 19, Appl
96	16	80.0	3	4	US-09-264-709A-5	Sequence 5, Appli
97	16	80.0	4	1	US-08-285-777-1	Sequence 1, Appli
98	16	80.0	4	2	US-08-612-785B-24	Sequence 24, Appl
99	16	80.0	4	4	US-08-703-675C-37	Sequence 37, Appl
100	16	80.0	4	4	US-08-617-267C-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1

US-08-304-585-10

; Sequence 10, Application US/08304585

; Patent No. 5721106

; GENERAL INFORMATION:

; APPLICANT: Maggio, John E.

; APPLICANT: Mantyh, Patrick W.

; TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND

; TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.

; STREET: P.O. Box 581415

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55458-1415

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/304,585

; FILING DATE: 12-SEP-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Mueting, Ann M.

; REGISTRATION NUMBER: 33,977

; REFERENCE/DOCKET NUMBER: 110.00010120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-304-585-10

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFF 4
|||
Db 1 LVFF 4

RESULT 11

US-08-127-904-15

; Sequence 15, Application US/08127904

; Patent No. 5470951

; GENERAL INFORMATION:

; APPLICANT: Eugene Roberts

; TITLE OF INVENTION: Method For Antagonizing

; TITLE OF INVENTION: Amnestic Effects of Amyloid n

; TITLE OF INVENTION: Protein and Improving the

; TITLE OF INVENTION: Quality of Life in Individuals

; TITLE OF INVENTION: With Alzheimer Disease

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: City of Hope

; STREET: 1500 East Duarte Road

; CITY: Duarte

; STATE: California

; COUNTRY: United States of America

; ZIP: 91010-0269

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3M Double Density 5 1/4" diskette

; COMPUTER: Wang PC

; OPERATING SYSTEM: MS DOS Version 3.20

; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,904
; FILING DATE: 29 September 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA: No. 5470951e
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
; REGISTRATION NUMBER: 16,541
; REFERENCE/DOCKET NUMBER: No. 5470951e
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; TELEX: No. 5470951e
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: Amino Acid
; STRANDEDNESS:
; TOPOLOGY: Unknown
US-08-127-904-15

Query Match 100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFF 4
|||
Db 2 LVFF 5

RESULT 22

US-08-970-833-2

; Sequence 2, Application US/08970833

; Patent No. 6022859

; GENERAL INFORMATION:

; APPLICANT: Kiessling, Laura L.

; APPLICANT: Murphy, Regina M.

; TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Quarles & Brady

; STREET: 411 East Wisconsin Avenue

; CITY: Milwaukee

; STATE: Wisconsin
 ; COUNTRY: U.S.A.
 ; ZIP: 53202-4497
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/970,833
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Baker, Jean C.
 ; REGISTRATION NUMBER: 35,433
 ; REFERENCE/DOCKET NUMBER: 960296.94291
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (414) 277-5709
 ; TELEFAX: (414) 271-3552
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-970-833-2

Query Match 100.0%; Score 20; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFF 4
 ||||
 Db 2 LVFF 5

Search completed: October 2, 2002, 08:27:05
 Job time: 132 sec

OM protein - protein search, using sw model

Run on: October 2, 2002, 08:22:53 ; Search time 14.08 Seconds
(without alignments)
27.298 Million cell updates/sec

Title: US-09-781-133-1
Perfect score: 20
Sequence: 1 LVFF 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 1099

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID	Description	
1	20	100.0	9	2	PT0080	60K Ca binding pro	
2	15	75.0	10	2	PT0310	Ig heavy chain CRD	

3	15	75.0	10 2	PH0807	T-cell receptor al
4	14	70.0	7 2	A30812	sex pheromone cCF1
5	13	65.0	9 2	B20569	serum amyloid P-co
6	13	65.0	10 2	B45482	platelet activatin
7	12	60.0	4 2	JQ1273	neuropeptide Antho
8	12	60.0	6 2	A60986	N-formyl oligopept
9	12	60.0	6 2	I59142	platelet-derived g
10	12	60.0	6 2	A43129	neuropeptide GNFFR
11	12	60.0	8 2	T13818	cytochrome oxidase
12	12	60.0	9 2	PT0315	Ig heavy chain CRD
13	12	60.0	9 2	B39504	octamer-binding pr
14	12	60.0	10 1	SPPGNK	neuromedin K - pig
15	12	60.0	10 2	S38304	lectin GNL1 alpha
16	12	60.0	10 2	A27617	triose-phosphate i
17	12	60.0	10 2	PN0165	triose-phosphate i
18	12	60.0	10 2	A58365	neuropeptide FFRFa
19	12	60.0	10 2	T13838	cytochrome-c oxida
20	12	60.0	10 2	T13976	cytochrome-c oxida
21	12	60.0	10 2	T17057	cytochrome-c oxida
22	12	60.0	10 2	T12303	cytochrome-c oxida
23	12	60.0	10 2	T14019	cytochrome-c oxida
24	12	60.0	10 2	T17060	cytochrome-c oxida
25	12	60.0	10 2	T14043	cytochrome-c oxida
26	12	60.0	10 2	T14054	cytochrome-c oxida
27	12	60.0	10 2	T17066	cytochrome-c oxida
28	12	60.0	10 2	T17069	cytochrome-c oxida
29	12	60.0	10 2	T12308	cytochrome-c oxida
30	12	60.0	10 2	T17072	cytochrome-c oxida
31	12	60.0	10 2	T12312	cytochrome-c oxida
32	12	60.0	10 2	T12316	cytochrome-c oxida
33	12	60.0	10 2	T12321	cytochrome-c oxida
34	12	60.0	10 2	T14219	cytochrome-c oxida
35	11	55.0	9 2	A61386	macrophage inhibit
36	11	55.0	10 2	PC2044	beta-Kirilowin - M
37	10	50.0	7 2	I40504	hypothetical prote
38	10	50.0	8 2	S08996	hypertrehalosemic
39	10	50.0	8 2	B49823	adipokinetic hormo
40	10	50.0	8 2	B44960	neuropeptide Led-C
41	10	50.0	8 2	A33995	adipokinetic hormo
42	10	50.0	8 2	S11545	adipokinetic hormo
43	10	50.0	9 2	A24244	adipokinetic hormo
44	10	50.0	9 2	D24180	fibrinogen beta ch
45	10	50.0	10 2	JC1416	hypertrehalosemic
46	10	50.0	10 2	S09138	hypertrehalosemic
47	10	50.0	10 2	A31571	hypertrehalosemic/

48	10	50.0	10 2	B33995	hypotrehalosemic h
49	10	50.0	10 2	S39374	mannose receptor -
50	10	50.0	10 2	A32543	cardioexcitatory n
51	10	50.0	10 2	A61617	ecdysteroid UDPglu
52	10	50.0	10 2	C39191	hypothetical prote
53	10	50.0	10 2	I44644	neurotoxin-associa
54	10	50.0	10 2	A56633	neomyosuppressin -
55	10	50.0	10 2	S66214	cartilage oligomer
56	10	50.0	10 4	S14943	UGA3 leader peptid
57	9	45.0	3 3	S68328	blood cell protein
58	9	45.0	5 2	PT0278	Ig heavy chain CRD
59	9	45.0	6 2	S11024	hydrogensulfite re
60	9	45.0	7 2	A25269	sex pheromone cAM3
61	9	45.0	7 2	S17976	glucose isomerase
62	9	45.0	7 2	E33932	Ig mu chain D regi
63	9	45.0	7 2	PX0008	glucuronosyltransf
64	9	45.0	8 2	S22428	chitin-binding pro
65	9	45.0	8 2	JS0318	leucokinin VIII -
66	9	45.0	8 2	B27867	homeotic protein U
67	9	45.0	8 2	B45800	serum albumin - do
68	9	45.0	8 2	PC4373	telomeric and tetr
69	9	45.0	8 2	A59028	MHC class I histoc
70	9	45.0	9 2	D58503	translation elonga
71	9	45.0	9 2	PD0443	3-oxoacid CoA-tran
72	9	45.0	9 2	S36850	Ig heavy chain V r
73	9	45.0	10 1	ECLQ1M	tachykinin I - mig
74	9	45.0	10 1	ECLQ3M	tachykinin III - m
75	9	45.0	10 2	A49581	sialokinin I - yel
76	9	45.0	10 2	B49581	sialokinin II - ye
77	9	45.0	10 2	A24867	scyliorhinin I - s
78	9	45.0	10 2	B61033	ranatachykinin B -
79	9	45.0	10 2	PT0230	Ig heavy chain CDR
80	9	45.0	10 2	PT0215	T-cell receptor be
81	8	40.0	3 3	PQ0010	angiotensin-conver
82	8	40.0	4 2	B43848	cell surface adhes
83	8	40.0	4 2	T46627	hypothetical prote
84	8	40.0	5 2	C41225	copper resistance
85	8	40.0	7 2	PQ0663	membrane protein -
86	8	40.0	7 2	PQ0728	unidentified 5.0/1
87	8	40.0	8 2	A37521	R-phycoerythrin ga
88	8	40.0	8 2	T10952	hypothetical prote
89	8	40.0	8 2	G33098	205K exoantigen -
90	8	40.0	8 2	A42057	fibroblast growth
91	8	40.0	8 2	PH0803	T-cell receptor al
92	8	40.0	8 2	S45651	probable Na ⁺ -trans

93	8	40.0	9	2	S10920	venom protein HR-3
94	8	40.0	10	2	A46491	C3 homolog HX - in
95	8	40.0	10	2	B43590	pilin type Ae6 - A
96	8	40.0	10	2	PC2172	triacylglycerol li
97	8	40.0	10	2	S13224	virG protein - Agr
98	8	40.0	10	2	I39702	nopaline synthase
99	8	40.0	10	2	S06964	hypothetical prote
100	8	40.0	10	2	A43590	pilin type Ae1 - A

ALIGNMENTS

RESULT 1

PT0080

60K Ca binding protein - edible frog (fragment)

C;Species: Rana esculenta (edible frog)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C;Accession: PT0080

R;Treveso, S.; Zorzato, F.; Chiozzi, P.; Melandri, P.; Volpe, P.; Pozzan, T.

Biochem. Biophys. Res. Commun. 175, 444-450, 1991

A;Title: Frog brain expresses a 60 kDa Ca²⁺ binding protein similar to mammalian calreticulin.

A;Reference number: PT0080; MUID:91207333

A;Accession: PT0080

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-9 <TRE>

Query Match 100.0%; Score 20; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFF 4

||||

Db 3 LVFF 6

RESULT 2

PT0310

Ig heavy chain CRD3 region (clone 6-97) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0310

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and joining segments in adult human peripheral blood B lymphocytes.

A;Reference number: PT0222; MUID:91108337

A;Accession: PT0310

A;Molecule type: DNA

A;Residues: 1-10 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 75.0%; Score 15; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 7.7e+02;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFF 4

||:

Db 3 LVWF 6

Search completed: October 2, 2002, 08:26:47

Job time: 234 sec

OM protein - protein search, using sw model

Run on: October 2, 2002, 08:26:48 ; Search time 10.14 Seconds
(without alignments)
15.274 Million cell updates/sec

Title: US-09-781-133-1
Perfect score: 20
Sequence: 1 LVFF 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 349

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match	Length	DB ID	Description
	Score	Match				
1	15	75.0	5	1	UC22_MAIZE	P80628 zea mays (m
2	14	70.0	7	1	CCF1_ENTFA	P20104 enterococcu
3	14	70.0	8	1	CPD1_ENTFA	P13269 enterococcu
4	14	70.0	10	1	RCA_PINPS	P81084 pinus pinas
5	13	65.0	8	1	UPAA_HUMAN	P30096 homo sapien

6	13	65.0	9	1	SAMP_MUSCA	P19095 mustelus ca
7	12	60.0	4	1	FFKA_ATEL	P58705 anthopleura
8	12	60.0	5	1	PAP2_PARMA	P81864 pardachirus
9	12	60.0	5	1	RE11_LITRU	P82070 litoria rub
10	12	60.0	5	1	RE21_LITRU	P82071 litoria rub
11	12	60.0	5	1	RE31_LITRU	P82072 litoria rub
12	12	60.0	5	1	RE32_LITRU	P82073 litoria rub
13	12	60.0	6	1	FARP_MONEX	P41966 moniezia ex
14	12	60.0	10	1	FARP_MYTED	P42560 mytilus edu
15	12	60.0	10	1	PAP1_PARMA	P81863 pardachirus
16	12	60.0	10	1	TKNK_PIG	P01292 sus scrofa
17	12	60.0	10	1	TKU2_UREUN	P40752 urechis uni
18	12	60.0	10	1	TPIS_NICPL	P19118 nicotiana p
19	12	60.0	10	1	TRP6_LEUMA	P81738 leucophaea
20	12	60.0	10	1	TRP7_LEUMA	P81739 leucophaea
21	11	55.0	9	1	FAR5_PANRE	P82661 panagrellus
22	10	50.0	8	1	AKH_TABAT	P14595 tabanus atr
23	10	50.0	8	1	HTF2_PERAM	P04549 periplaneta
24	10	50.0	8	1	PPK3_PERAM	P82618 periplaneta
25	10	50.0	9	1	FIBB_ERYPA	P19346 erythrocebu
26	10	50.0	10	1	FARP_LOCFI	P38553 locusta mig
27	10	50.0	10	1	HTF2_CARMO	P11385 carausius m
28	10	50.0	10	1	HTF_HELZE	P16353 heliothis z
29	10	50.0	10	1	HTF_TABAT	P14596 tabanus atr
30	10	50.0	10	1	LCMS_LEUMA	P21144 leucophaea
31	10	50.0	10	1	NEMS_DROME	P41494 drosophila
32	9	45.0	4	1	FYRI_ATEL	P58706 anthopleura
33	9	45.0	7	1	CIA_ENTFA	P11932 enterococcu
34	9	45.0	8	1	LCK8_LEUMA	P19990 leucophaea
35	9	45.0	8	1	NS3_MYCTU	P81152 mycobacteri
36	9	45.0	9	1	NEUU_CAVPO	P34966 cavia porce
37	9	45.0	9	1	NEUX_HUMAN	P04277 homo sapien
38	9	45.0	9	1	OXYF_SCYCA	P42997 scyliorhinu
39	9	45.0	9	1	OXYT_OCTVU	P80027 octopus vul
40	9	45.0	9	1	TKC1_CALVO	P41517 calliphora
41	9	45.0	9	1	TKL1_LOCFI	P16223 locusta mig
42	9	45.0	10	1	ANG1_BOTJA	Q10581 bothrops ja
43	9	45.0	10	1	GON1_CHEPR	P80677 chelyosoma
44	9	45.0	10	1	TKL2_LOCFI	P16224 locusta mig
45	9	45.0	10	1	TKL3_LOCFI	P30249 locusta mig
46	9	45.0	10	1	TKN1_SCYCA	P08608 scyliorhinu
47	9	45.0	10	1	TKNB_RANCA	P22689 rana catesb
48	9	45.0	10	1	TKS1_AEDAE	P42634 aedes aegyp
49	9	45.0	10	1	TKS2_AEDAE	P42635 aedes aegyp
50	8	40.0	7	1	UN06_PINPS	P81675 pinus pinas

51	8	40.0	8	1	CAD1_ENTFA	P13268 enterococcu
52	8	40.0	9	1	ULAD_HUMAN	P31929 homo sapien
53	8	40.0	9	1	UPA7_HUMAN	P30093 homo sapien
54	8	40.0	10	1	AKHX_LOCFI	P81626 locusta mig
55	8	40.0	10	1	NS1_MYCTU	P81135 mycobacteri
56	8	40.0	10	1	UPA5_HUMAN	P30091 homo sapien
57	8	40.0	10	1	UXA2_CHLTR	P38003 chlamydia t
58	7	35.0	4	1	FAR3_HIRME	P42562 hirudo medi
59	7	35.0	4	1	FLRF_HIRME	P42561 hirudo medi
60	7	35.0	6	1	CIP1_MYTED	P13736 mytilus edu
61	7	35.0	6	1	CIP2_MYTED	P13737 mytilus edu
62	7	35.0	7	1	FAR1_HELTI	P41871 helisoma tr
63	7	35.0	7	1	FAR1_PROCL	P38499 procambarus
64	7	35.0	7	1	FAR2_ASCSU	P31890 ascaris suu
65	7	35.0	7	1	FAR2_PROCL	P38498 procambarus
66	7	35.0	7	1	GFRP_MOUSE	P99025 mus musculu
67	7	35.0	7	1	TY51_LITRU	P82065 litoria rub
68	7	35.0	8	1	AKHG_GRYBI	P14086 gryllus bim
69	7	35.0	8	1	AKH_LIBAU	P25418 libellula a
70	7	35.0	8	1	ANG2_BOTJA	Q10582 bothrops ja
71	7	35.0	8	1	COXG_RAT	P80430 rattus norv
72	7	35.0	8	1	FAR1_PANRE	P41872 panagrellus
73	7	35.0	8	1	FAR3_HOMAM	P41486 homarus ame
74	7	35.0	8	1	FAR4_HOMAM	P41487 homarus ame
75	7	35.0	8	1	HTF1_PERAM	P04548 periplaneta
76	7	35.0	8	1	HTF_TENMO	P25419 tenebrio mo
77	7	35.0	8	1	NPB_BOVIN	P15507 bos taurus
78	7	35.0	8	1	RPCH_PANBO	P08939 pandalus bo
79	7	35.0	9	1	BUK_CLOPA	P81337 clostridium
80	7	35.0	9	1	D1_NEPNO	P24816 nephrops no
81	7	35.0	9	1	DNF1_LOCFI	P16339 locusta mig
82	7	35.0	9	1	FAR2_PANRE	P41873 panagrellus
83	7	35.0	9	1	FAR9_ASCSU	P43172 ascaris suu
84	7	35.0	9	1	FARP_CALSI	P38495 callinectes
85	7	35.0	9	1	FIBB_MACFU	P19345 macaca fusc
86	7	35.0	9	1	FIBB_PAPAN	P19344 papio anubi
87	7	35.0	9	1	FIBB_PAPHA	P19343 papio hamad
88	7	35.0	9	1	FIBB_THEGE	P19342 theropithec
89	7	35.0	9	1	FLA2_TREHY	P80159 treponema h
90	7	35.0	9	1	MOSF_CLYJA	P19853 clypeaster
91	7	35.0	9	1	MOSH_CLYJA	P19852 clypeaster
92	7	35.0	9	1	ULAE_HUMAN	P31931 homo sapien
93	7	35.0	9	1	UPA3_HUMAN	P30089 homo sapien
94	7	35.0	10	1	ANGT_BOVIN	P01017 bos taurus
95	7	35.0	10	1	ANGT_CHICK	P01018 gallus gall

96	7	35.0	10	1	APE_CAPGI	P80474 capnocytoph
97	7	35.0	10	1	CA12_LITCI	P82086 litoria cit
98	7	35.0	10	1	FAR6_PANRE	P82660 panagrellus
99	7	35.0	10	1	FARP_MANSE	P18523 manduca sex
100	7	35.0	10	1	GS09_BACSU	P80243 bacillus su

ALIGNMENTS

RESULT 1

UC22_MAIZE

ID UC22_MAIZE STANDARD; PRT; 5 AA.

AC P80628;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Unknown protein from 2D-page of etiolated coleoptile (Spot 474)

DE (Fragment).

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;

OC Panicoideae; Andropogoneae; Zea.

OX NCBI_TaxID=4577;

RN [1]

RP SEQUENCE.

RC TISSUE=Coleoptile;

RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,

RA Pernollet J.-C., Zivy M., de Vienne D.;

RT "The maize two dimensional gel protein database: towards an integrated

RT genome analysis program.";

RL Theor. Appl. Genet. 93:997-1005(1996).

CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa.

DR Maize-2DPAGE; P80628; COLEOPTILE.

DR MaizeDB; 123954; -.

FT NON_TER 1 1

FT NON_TER 5 5

SQ SEQUENCE 5 AA; 654 MW; 72CB19C9C0300000 CRC64;

Query Match 75.0%; Score 15; DB 1; Length 5;

Best Local Similarity 66.7%; Pred. No. 1e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VFF 4

:||
Db 1 IFF 3

Search completed: October 2, 2002, 08:30:20

Job time: 212 sec

GenCore version 4.5

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OM protein - protein search, using sw model

Run on: October 2, 2002, 08:26:28 ; Search time 23.82 Seconds
(without alignments)
29.050 Million cell updates/sec

Title: US-09-781-133-1
Perfect score: 20
Sequence: 1 LVFF 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 1088

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SPTREMBL_19:*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertibrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query				DB ID	Description
	Score	Match	Length			
1	18	90.0	9	8	Q9GD36	Q9gd36 juncus effu
2	17	85.0	10	12	O39952	O39952 hepatitis g
3	17	85.0	10	12	Q9WLE4	Q9wle4 hepatitis g
4	16	80.0	9	10	P82440	P82440 nicotiana t
5	15	75.0	8	3	O13591	O13591 saccharomyc
6	15	75.0	9	2	O30790	O30790 erwinia amy
7	14	70.0	9	8	Q94VG2	Q94vg2 varanus ind
8	13	65.0	8	10	Q40530	Q40530 nicotiana t
9	12	60.0	5	13	P82070	P82070 litoria rub
10	12	60.0	5	13	P82071	P82071 litoria rub
11	12	60.0	5	13	P82072	P82072 litoria rub
12	12	60.0	5	13	P82073	P82073 litoria rub
13	12	60.0	8	8	Q9TD02	Q9td02 terranatos
14	12	60.0	8	8	Q9T4Y2	Q9t4y2 asterina pe
15	12	60.0	8	11	Q99NX9	Q99nx9 hydrochoeru
16	12	60.0	9	4	Q99887	Q99887 homo sapien
17	12	60.0	9	8	Q9T688	Q9t688 gecko gecko
18	12	60.0	10	2	Q9XBH3	Q9xbh3 bacillus ce
19	12	60.0	10	2	Q9AE19	Q9ae19 streptococc
20	12	60.0	10	8	Q9T4P9	Q9t4p9 liolaemus d
21	12	60.0	10	8	Q9ZYV3	Q9zyv3 dipsosaurus
22	12	60.0	10	8	Q9ZYV0	Q9zyv0 petrosaurus
23	12	60.0	10	8	Q9ZYU7	Q9zyu7 sator angus
24	12	60.0	10	8	Q9ZYU4	Q9zyu4 sceloporus
25	12	60.0	10	8	Q9ZYU1	Q9zyu1 uma scopari
26	12	60.0	10	8	Q9ZYT8	Q9zyt8 urosaurus g
27	12	60.0	10	8	Q9ZYT5	Q9zyt5 uta stansbu
28	12	60.0	10	8	Q9ZYS9	Q9zys9 phymaturus
29	12	60.0	10	8	Q9TG98	Q9tg98 shinisaurus
30	12	60.0	10	8	Q9TFU9	Q9tfu9 teratoscinc
31	12	60.0	10	8	Q9TFU6	Q9tfu6 teratoscinc
32	12	60.0	10	8	P92758	P92758 teratoscinc
33	12	60.0	10	8	P92648	P92648 lialis jica

34	12	60.0	10 8	P92707	P92707 platysaurus
35	12	60.0	10 8	P92654	P92654 mabuya aura
36	12	60.0	10 8	P92632	P92632 eremias gra
37	12	60.0	10 8	P92616	P92616 cnemidophor
38	12	60.0	10 8	P92771	P92771 xenosaurus
39	12	60.0	10 8	P92576	P92576 bipes bipor
40	12	60.0	10 8	O79885	O79885 anolis pate
41	12	60.0	10 8	O79891	O79891 crotaphytus
42	12	60.0	10 8	O79894	O79894 gambelia wi
43	12	60.0	10 8	O79900	O79900 liolaemus p
44	12	60.0	10 8	O79903	O79903 oplurus cuv
45	12	60.0	10 8	O79906	O79906 phrynosoma
46	12	60.0	10 8	O79909	O79909 sauromalus
47	12	60.0	10 8	Q9T8X7	Q9t8x7 phymaturus
48	12	60.0	10 8	Q9T8X4	Q9t8x4 liolaemus c
49	12	60.0	10 8	Q9T8W8	Q9t8w8 liolaemus b
50	12	60.0	10 8	Q9T8W2	Q9t8w2 liolaemus b
51	12	60.0	10 8	Q9T8V9	Q9t8v9 liolaemus g
52	12	60.0	10 8	Q9T8V6	Q9t8v6 liolaemus b
53	12	60.0	10 8	Q9T8V3	Q9t8v3 liolaemus c
54	12	60.0	10 8	Q9T8V0	Q9t8v0 liolaemus c
55	12	60.0	10 8	Q9T8U8	Q9t8u8 liolaemus p
56	12	60.0	10 8	Q9T8U5	Q9t8u5 liolaemus z
57	12	60.0	10 8	Q9T8U2	Q9t8u2 liolaemus t
58	12	60.0	10 8	Q9T8T9	Q9t8t9 liolaemus l
59	12	60.0	10 8	Q9T8T6	Q9t8t6 liolaemus m
60	12	60.0	10 8	Q9T8T3	Q9t8t3 liolaemus n
61	12	60.0	10 8	Q9T8T0	Q9t8t0 liolaemus f
62	12	60.0	10 8	Q9T8S7	Q9t8s7 liolaemus n
63	12	60.0	10 8	Q9T8S4	Q9t8s4 liolaemus c
64	12	60.0	10 8	Q9T8S1	Q9t8s1 liolaemus l
65	12	60.0	10 8	Q9T8R9	Q9t8r9 liolaemus b
66	12	60.0	10 8	Q9T8R7	Q9t8r7 liolaemus c
67	12	60.0	10 8	Q9T8R4	Q9t8r4 liolaemus p
68	12	60.0	10 8	Q9T8R1	Q9t8r1 liolaemus a
69	12	60.0	10 8	Q9T8Q8	Q9t8q8 liolaemus e
70	12	60.0	10 8	Q9T8Q5	Q9t8q5 liolaemus l
71	12	60.0	10 8	Q9T8Q2	Q9t8q2 liolaemus s
72	12	60.0	10 8	Q9T8P9	Q9t8p9 liolaemus m
73	12	60.0	10 8	Q9T8P6	Q9t8p6 liolaemus r
74	12	60.0	10 8	Q9T8N4	Q9t8n4 liolaemus d
75	12	60.0	10 8	Q9T8N1	Q9t8n1 liolaemus p
76	12	60.0	10 8	Q9T8M8	Q9t8m8 liolaemus m
77	12	60.0	10 8	Q9T8M5	Q9t8m5 liolaemus a
78	12	60.0	10 8	Q9T8M2	Q9t8m2 liolaemus c

79	12	60.0	10	8	Q9T8L6	Q9t8l6 liolaemus p
80	12	60.0	10	8	Q9T8L3	Q9t8l3 liolaemus l
81	12	60.0	10	8	Q9T8L0	Q9t8l0 liolaemus o
82	12	60.0	10	8	Q9T8K7	Q9t8k7 liolaemus m
83	12	60.0	10	8	Q9T8K4	Q9t8k4 liolaemus s
84	12	60.0	10	8	Q9T8K1	Q9t8k1 liolaemus s
85	12	60.0	10	8	Q9T8J8	Q9t8j8 liolaemus w
86	12	60.0	10	8	Q9T8J5	Q9t8j5 liolaemus m
87	12	60.0	10	8	Q9T8J2	Q9t8j2 liolaemus r
88	12	60.0	10	8	Q9T8I9	Q9t8i9 liolaemus a
89	12	60.0	10	8	Q9T8I6	Q9t8i6 liolaemus k
90	12	60.0	10	8	Q9T8I3	Q9t8i3 liolaemus q
91	12	60.0	10	8	Q9T8I0	Q9t8i0 liolaemus o
92	12	60.0	10	8	Q9T8H7	Q9t8h7 liolaemus a
93	12	60.0	10	8	Q9T8H4	Q9t8h4 liolaemus i
94	12	60.0	10	8	Q9T8H1	Q9t8h1 liolaemus u
95	12	60.0	10	8	Q9T8G8	Q9t8g8 liolaemus c
96	12	60.0	10	8	Q9T8G5	Q9t8g5 liolaemus o
97	12	60.0	10	8	Q9T8G0	Q9t8g0 liolaemus l
98	12	60.0	10	8	Q9T8F5	Q9t8f5 liolaemus b
99	12	60.0	10	8	Q958L8	Q958l8 rana catesb
100	12	60.0	10	8	Q958L5	Q958l5 rana sylvat

ALIGNMENTS

RESULT 1

Q9GD36

ID Q9GD36 PRELIMINARY; PRT; 9 AA.

AC Q9GD36;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE RIBOSOMAL PROTEIN S16 (FRAGMENT).

GN RPS16.

OS *Juncus effusus*.

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Juncaceae; *Juncus*.

OX NCBI_TaxID=13579;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LEAF;

RA Asmussen C.B., Chase M.W.;

RT "Coding and noncoding plastid DNA in palm systematics.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ404962; CAC17904.1; -.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1135 MW; 8DCCC9D2C046CB41 CRC64;

Query Match 90.0%; Score 18; DB 8; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFF 4
:||||
Db 5 IVFF 8

Search completed: October 2, 2002, 08:30:03
Job time: 215 sec